

Refine Search

Search Results -

Terms	Documents
"Esikova, Irina"[IN]	3

Database:

US Pre-Grant Publication Full-Text Database
 US Patents Full-Text Database
 US OCR Full-Text Database
 EPO Abstracts Database
 JPO Abstracts Database
 Derwent World Patents Index
 IBM Technical Disclosure Bulletins

Search:

L9

Search History

DATE: Wednesday, September 13, 2006

[Purge Queries](#)
[Printable Copy](#)
[Create Case](#)

<u>Set</u> <u>Name</u> side by side	<u>Query</u>	<u>Hit</u> <u>Count</u>	<u>Set</u> <u>Name</u> result set
<i>DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; PLUR=YES; OP=OR</i>			
L9	"Esikova, Irina"[IN]	3	L9
L8	"Fordham, Dennis"[IN]	2	L8
L7	"Babuka, Susan"[IN]	7	L7
L6	"Shirley, Bret"[IN]	24	L6
L5	"Wolfe, Sidney"[IN]	13	L5
L4	L1 same (guanidine and (ethanol or propanol or alcohol) same (filtration or dialy\$6))	18	L4
L3	L1 same guanidine and (ethanol or propanol or alcohol) same (filtration or dialy\$6)	40	L3
L2	L1 and guanidine and (ethanol or propanol or alcohol) and (filtration or dialy\$6)	6439	L2
L1	(interferon or IFN or INF)	87511	L1

FILE 'MEDLINE, BIOSIS, EMBASE, SCISEARCH, CAPLUS, USPATFULL, PCTFULL'
ENTERED AT 19:06:14 ON 13 SEP 2006

L1 663358 S (INTERFERON OR IFN OR INF)
L2 1495 S L1(P) (GUANIDINE) (P) (ETHANOL OR PROPANOL OR ALCOHOL) (P) (DIALY?
L3 1492 DUP REM L2 (3 DUPLICATES REMOVED)
L4 645 S L3 AND PY<2001
L5 7 S L1(S) (GUANIDINE) (S) (ETHANOL OR PROPANOL OR ALCOHOL) (S) (DIALY?
L6 45 S L1(S) (GUANIDINE) (S) (DIALY? OR FILTRATION)
L7 3 S WOLFE, SIDNEY/IN
L8 6 S SHIRLEY, BRET/IN
L9 10 S BABUKA, SUSAN/IN
L10 4 S FORDHAM, DENNIS/IN
L11 7 S ESIKOVA, IRINA/IN

=>

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OM protein - protein search, using sw model

Run on: August 30, 2006, 08:20:47 ; Search time 71.5 Seconds
(without alignments)
1061.509 Million cell updates/sec

Title: US-10-750-076-1
Perfect score: 874
Sequence: 1 MSYNLLGFLQRSSNFQCQKL.....RVEILRNFYFINRLTGYLRN 166

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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OM protein - protein search, using sw model

Run on: August 30, 2006, 08:23:37 ; Search time 17 Seconds
(without alignments)
854.711 Million cell updates/sec

Title: US-10-750-076-1
Perfect score: 874
Sequence: 1 MSYNLLGFLQRSSNFQCQKL.....RVEILRNFYFINRLTGYLRLN 166

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

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OM protein - protein search, using sw model

Run on: August 30, 2006, 08:23:55 ; Search time 48 Seconds
(without alignments)
1601.951 Million cell updates/sec

Title: US-10-750-076-1
Perfect score: 874
Sequence: 1 MSYNLLGFLQRSSNFQCQKL.....RVEILRNFYFINRLTGYLRLN 166

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

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OM protein - protein search, using sw model

Run on: August 30, 2006, 08:24:33 ; Search time 10 Seconds
(without alignments)
1143.291 Million cell updates/sec

Title: US-10-750-076-1
Perfect score: 874
Sequence: 1 MSYNLLGFLQRSSNFQCQKL.....RVEILRNFYFINRLTGYLRN 166

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 250042 seqs, 68872936 residues

Total number of hits satisfying chosen parameters: 250042

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

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OM protein - protein search, using sw model

Run on: August 30, 2006, 08:22:55 ; Search time 13 Seconds
(without alignments)
1228.614 Million cell updates/sec

Title: US-10-750-076-1
Perfect score: 874
Sequence: 1 MSYNLLGFLQRSSNFQCQKL.....RVEILRNFYFINRLTGYLRLN 166

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

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OM protein - protein search, using sw model

Run on: August 30, 2006, 08:22:06 ; Search time 90 Seconds
(without alignments)
1706.140 Million cell updates/sec

Title: US-10-750-076-1
Perfect score: 874
Sequence: 1 MSYNLLGFLQRSSNFQCQKL.....RVEILRNIFYFINRLTGYLRLN 166

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

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OM protein - protein search, using sw model

Run on: August 30, 2006, 08:20:47 ; Search time 71.5 Seconds
(without alignments)
1061.509 Million cell updates/sec

Title: US-10-750-076-2
Perfect score: 869
Sequence: 1 MSYNLLGFLQRSSNFQSQKL.....RVEILRNFYFINRLTGYLRN 166

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: geneseqp2001s:*
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3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

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- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

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